Fig. 1: Identification of differentially expressed genes in a fluorescence differential display screen

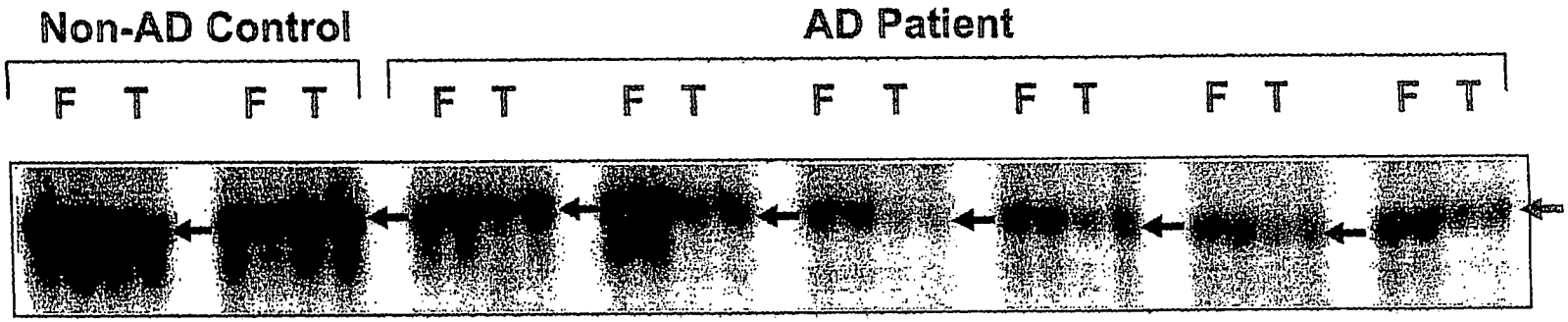
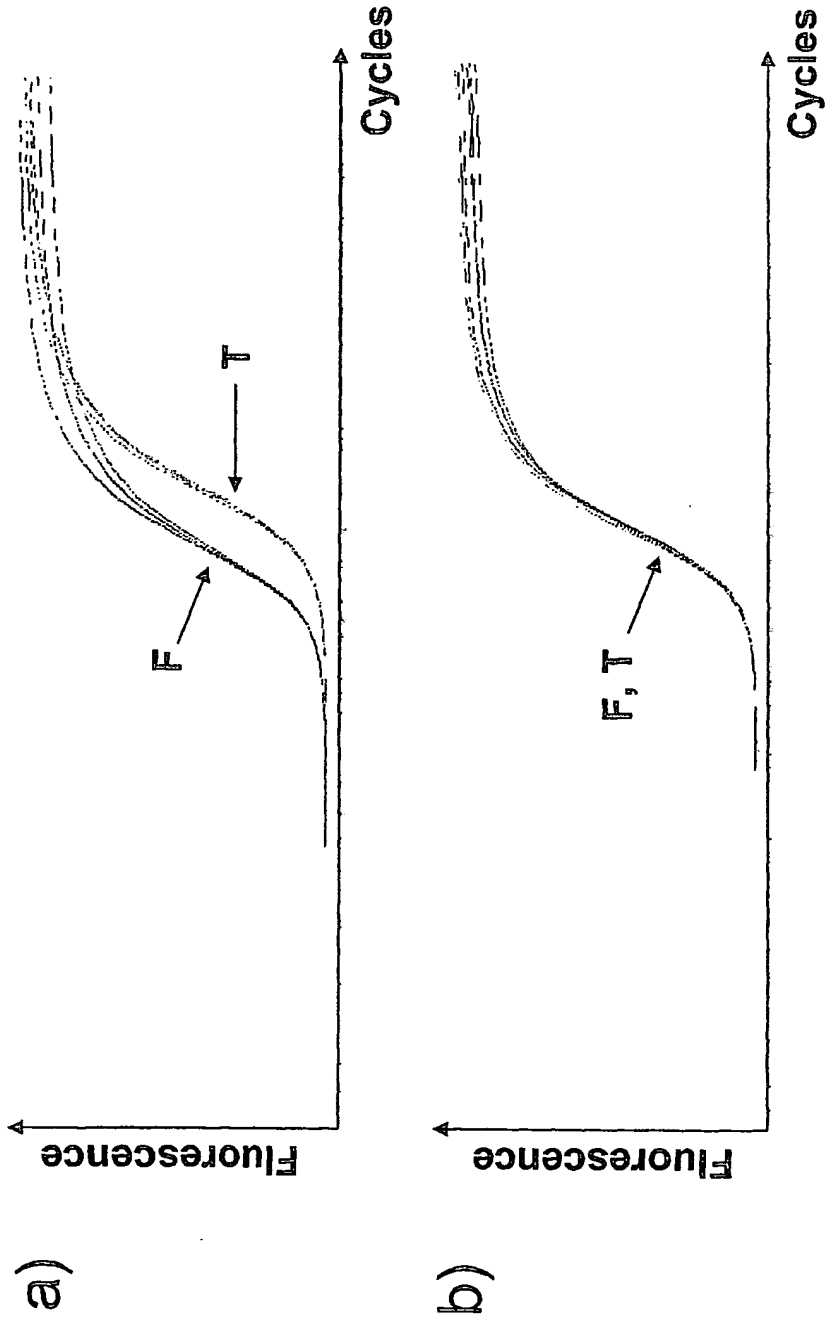


Fig. 2: Verification of differential expression of SULT4A1 splice variant 1 and/or splice variant 2 by quantitative RT-PCR



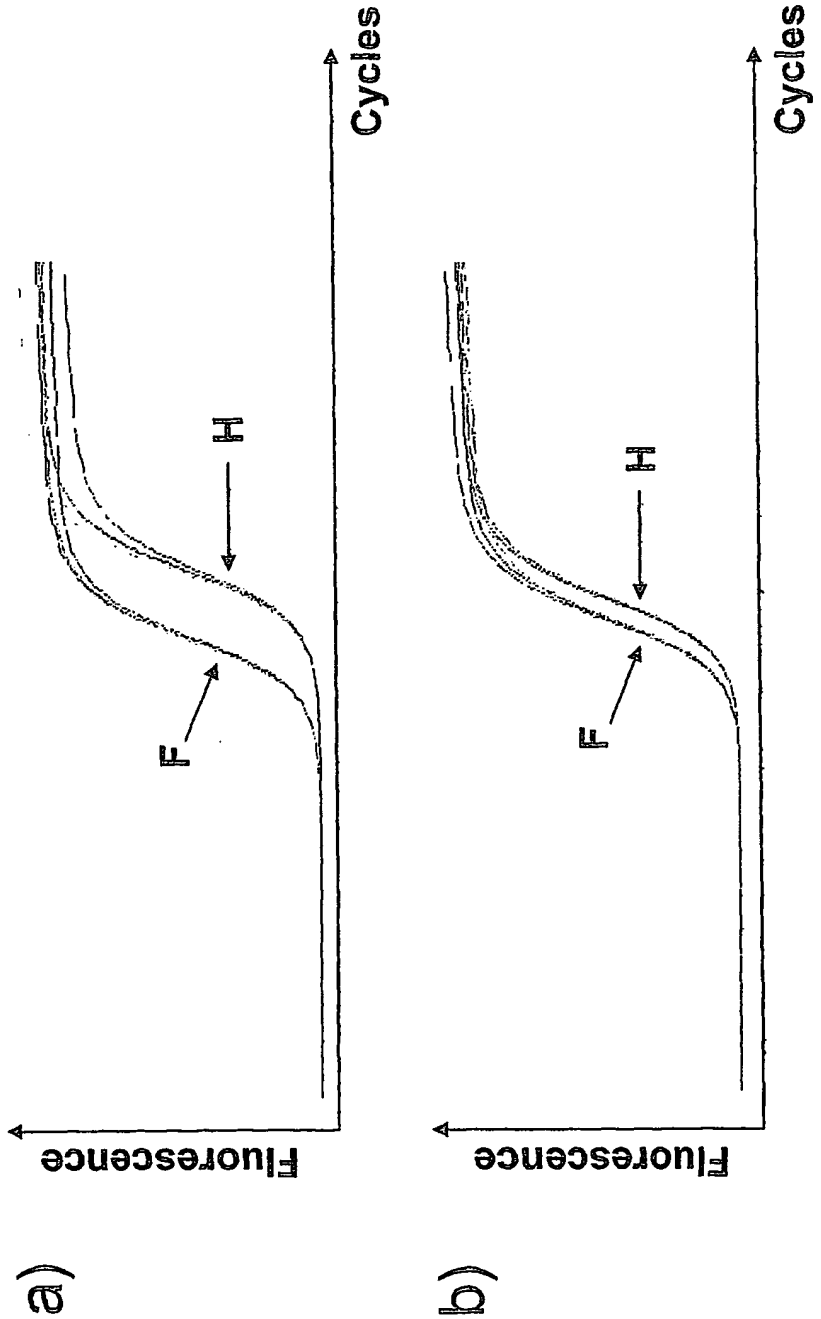


Fig. 3: Verification of differential expression of SULT4A1 splice variant 1 and/or splice variant 2 by quantitative RT-PCR

Fig. 4: Verification of differential expression of SULT4A1 splice variant 1 by quantitative RT-PCR

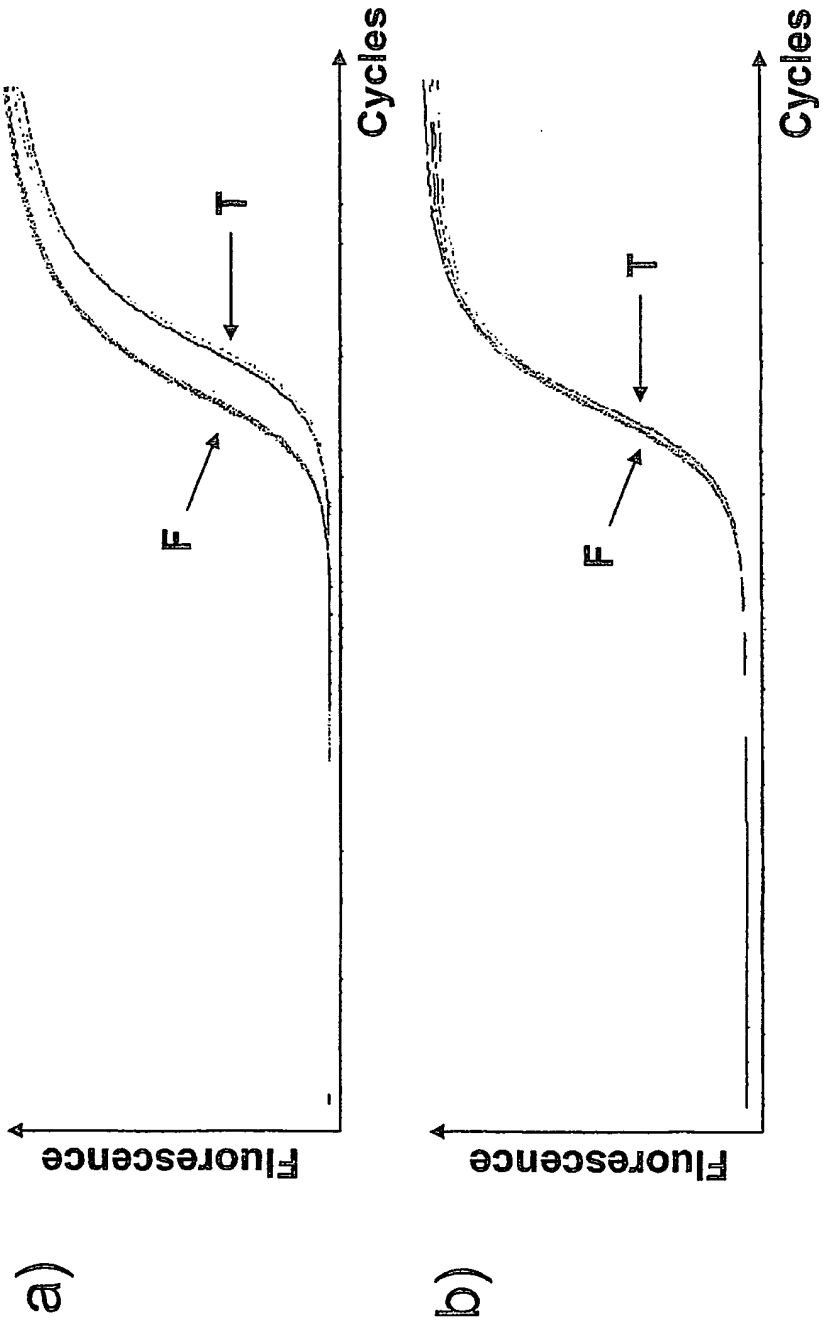


Fig. 5: Verification of differential expression of SULT4A1 splice variant 2 by quantitative RT-PCR

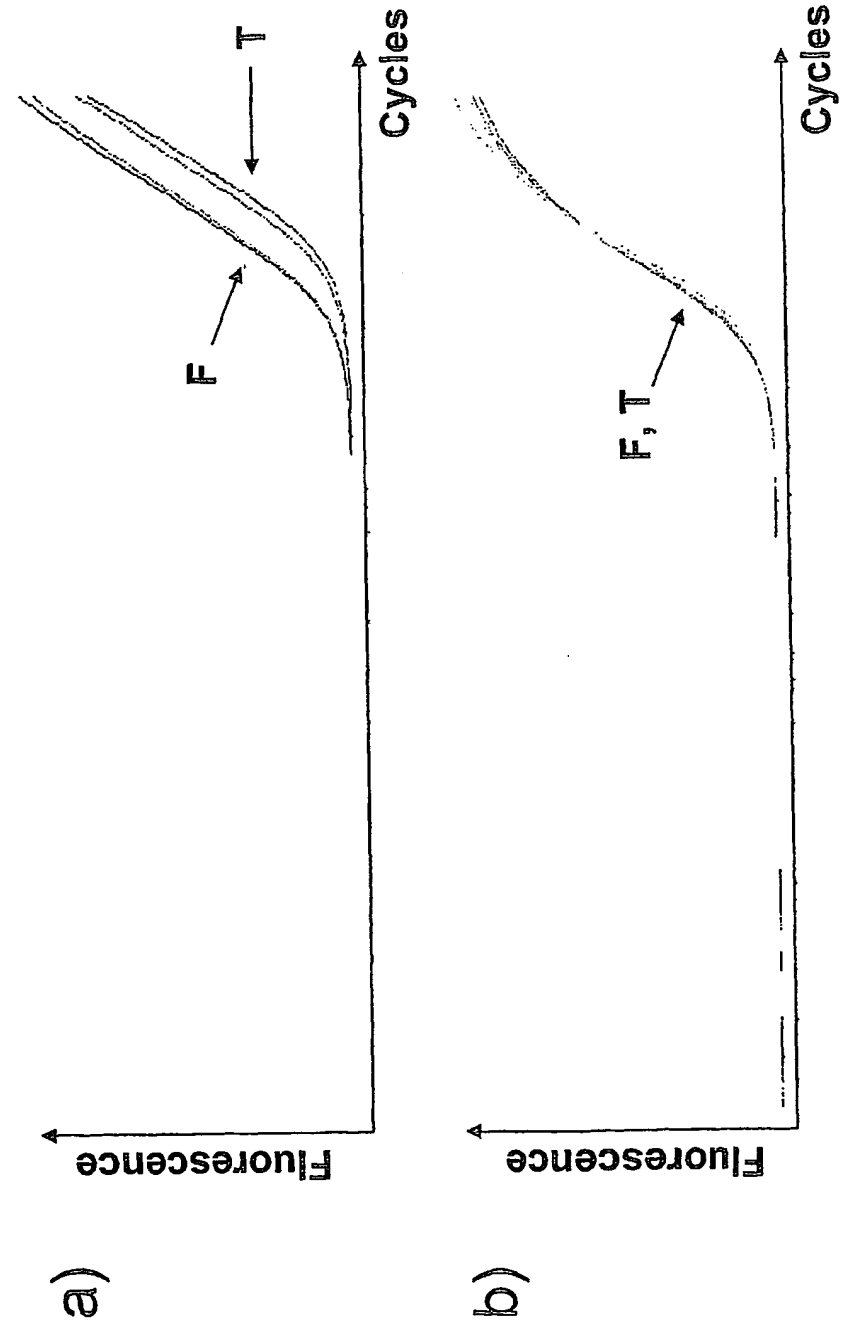
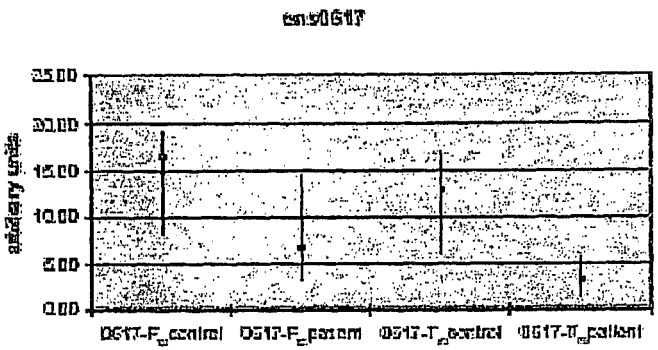
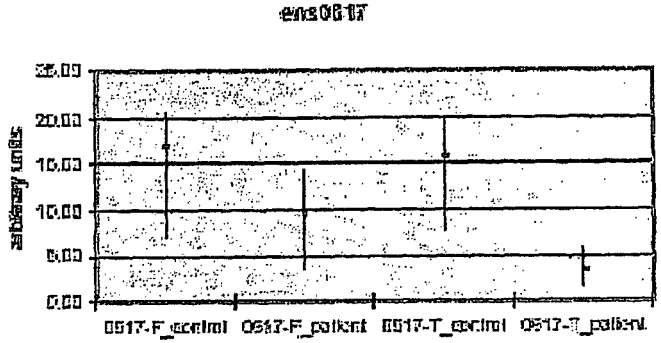


Fig. 6: Analysis of absolute mRNA expression of SULT4A1sv1 and/or SULT4A1sv2

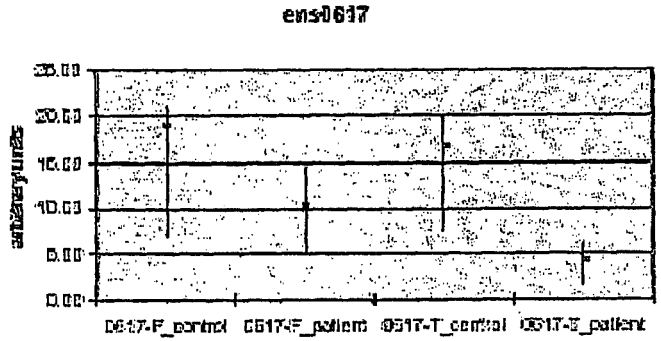
Comparison of Braak 0-3 with 4-6



Comparison of Braak 0-2 with Braak 3-6



Comparison of Braak 0-1 with 2-6



Comparison of Braak 0-1 with 2-3 and 4-6

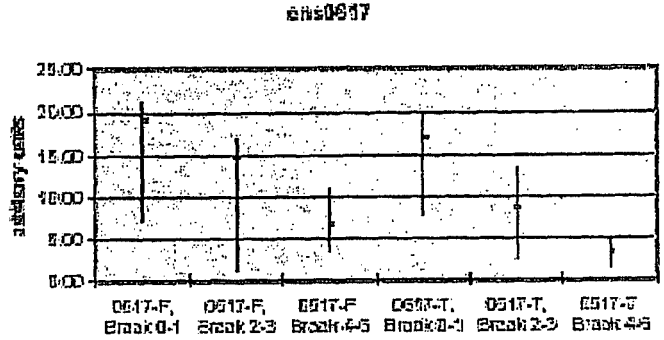
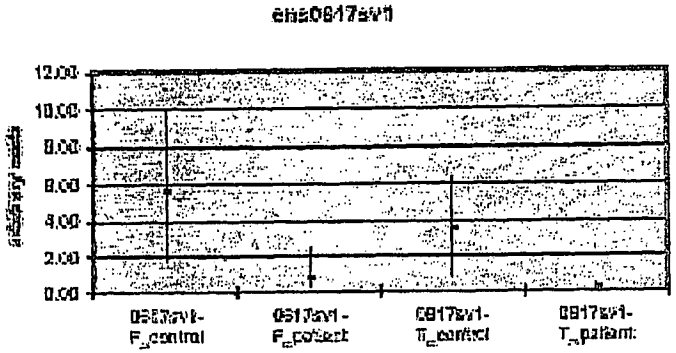
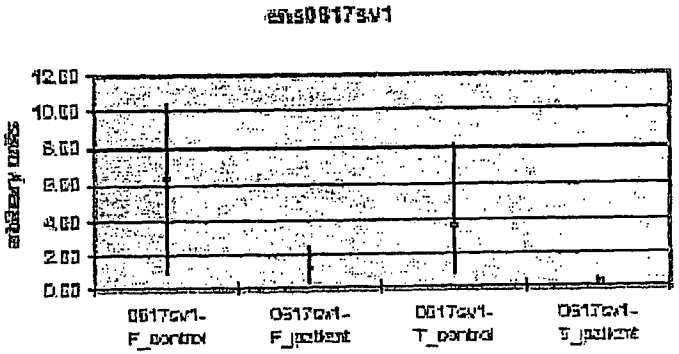


Fig. 7: Analysis of absolute mRNA expression of SULT4A1sv1

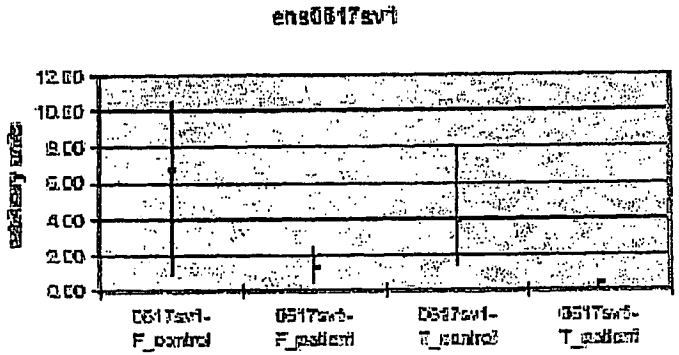
Comparison of Braak 0-3 with 4-6



Comparison of Braak 0-2 with Braak 3-6



Comparison of Braak 0-1 with 2-6



Comparison of Braak 0-1 with 2-3 and 4-6

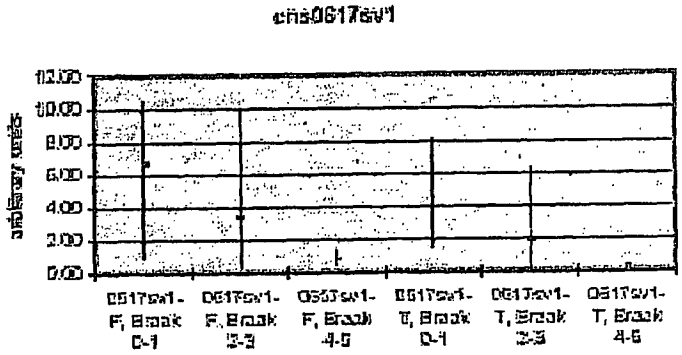


Fig. 8: SEQ ID NO. 1: amino acid sequence of human SULT4A1 protein, splice variant 1

Length: 284 aa

```
  1  MAESEAETPS TPGEFESKYF EFHGVRLPPF CRGKMEEIAN FPVRPSDVWI
 51  VTYPKSGTSL LQEVVYLVSQ GADPDEIGLM NIDEQLPVLE YPQPGLDIIK
101  ELTSPRLIKS HLPYRFLPSD LHNGDSKVIY MARNPKDLVV SYYQFHRSLR
151  TMSYRGTFQE FCRRFMNDKL GYGSWFEHVQ EFWEHRMDSN VLFLKYEDMH
201  RDLVTMVEQL ARFLGVSCDK AQLEALTEHC HQLVDQCCNA EALPVGRGRV
251  GLWKDIFTVS MNEKFDLVYK QKMGKCDLTF DFYL
```

Fig. 9: SEQ ID NO. 2:
amino acid sequence of human SULT4A1 protein, splice variant 2

Length: 171 aa

```
  1  MAESEAETPS TPGEFESKYF EFHGVRLPPF CRGKMEEIAN FPVRPSDVWI
 51  VTYPKSVGYG SWFEHVQEFW EHRMDSNVLF LKYEDMHRDL VTMVEQLARF
101  LGVSCDKAQL EALTEHCHQL VDQCCNAEAL PVGRGRVGLW KDIFTVSMNE
151  KFDLVYKQKM GKCDLTFDFY L
```

Fig. 10: SEQ ID NO. 3: nucleotide sequence of human SULT4A1 cDNA, splice variant 1

Length: 2419 bp

```
   1 GCGACGGCGA CGGCGGCGGC ATGGCGGAGA GCGAGGCCGA GACCCCCAGC
  51 ACCCCGGGGG AGTTCGAGAG CAAGTACTTC GAGTTCCATG GCGTGCGGCT
 101 GCCGCCCTTC TGCCGCGGGA AGATGGAGGA GATCGCCAAC TTCCCGGTGC
 151 GGCCCAGCGA CGTGTGGATC GTCACCTACC CCAAGTCCGG CACCAGCTTG
 201 CTGCAGGAGG TGGTCTACTT GGTGAGCCAG GGCGCTGACC CCGATGAGAT
 251 CGGCTTGATG AACATCGACG AGCAGCTCCC GGTCCTGGAG TACCCACAGC
 301 CGGGCCTGGA CATCATCAAG GAACTGACCT CTCCCCGCCT CATCAAGAGC
 351 CACCTGCCCT ACCGCTTTCT GCCCTCTGAC CTCCACAATG GAGACTCCAA
 401 GGTCATCTAT ATGGCTCGCA ACCCCAAGGA TCTGGTGGTG TCTTATTATC
 451 AGTTCCACCG CTCTCTGCGG ACCATGAGCT ACCGAGGCAC CTTTCAAGAA
 501 TTCTGCCGGA GGTTTATGAA TGATAAGCTG GGCTACGGCT CCTGGTTTGA
 551 GCACGTGCAG GAGTTCTGGG AGCACCGCAT GGACTCGAAC GTGCTTTTTC
 601 TCAAGTATGA AGACATGCAT CGGGACCTGG TGACGATGGT GGAGCAGCTG
 651 GCCAGATTCC TGGGGGGTGTC CTGTGACAAG GCCCAGCTGG AAGCCCTGAC
 701 GGAGCACTGC CACCAGCTGG TGGACCAGTG CTGCAACGCT GAGGCCCTGC
 751 CCGTGGGCCG GGGAAGAGTT GGGCTGTGGA AGGACATCTT CACCGTCTCC
 801 ATGAATGAGA AGTTTGACTT GGTGTATAAA CAGAAGATGG GAAAGTGTGA
 851 CCTCACGTTT GACTTTTATT TATAATAACA GAAACAACAA CCTGCATGCT
 901 CACAATACCC AGACAGTCTA CTAGCCAAAA GTCCTGTATG CATTCATTTA
 951 TTCCTTGCTG GACAAACTCT GGAAGCAGCG TGTGAAACAG CGGGGGAAGG
1001 GAAGAGCGGC GTGAGCGGAG GGAGTGTGAT GATTCCCAAC CGAAGCAGCT
1051 GTCTCGCCTT TAGAACGTGC AGCCTCTCCA TGTCTGATTA CAAACAGTCT
1101 CCACATTGCA GTTCCAATGG CCTGGACCGT AAGGATAAAG CCTGTAATAT
1151 ATGCAACTAG AATGTCTGCC TTTTCAACCC CGTATTATTG TATTTTATAG
1201 AGCTTTTCAC TGGAAATCTA CATAAATGTC AGTAAACCAA ATAAAAGTTC
1251 ATTTCCAAGG GGAATCAGGA GCGAGCCACA CCCGAATGGT AGAAAGATCT
1301 CAGGGTTAAC TCTTTATTTT TGTAGTTTTA TTATCTAAGG CACAGCCATT
1351 CTGTTCTCAC TTGGTTCTGA GATAGTGGTG AGAACAGAGG ATGAGTTGGG
1401 TCTGTTGGGG GGAATCTGGA CACTTGTTTA TTCTGACGGA GTTCACTTCT
1451 TCAGAACCTT CCTGAAATGA GCAGAAATTG TTCACTAGGT CTTCAGAATG
1501 GACGTCCTTC TGCCAGAGAC TTCCAGCGGG CGGCTCCAAA GGCCCAATGC
1551 AGAGGAGCCC GCGGAGCATG TGCTGAGGGA AGTCTGCCTG GTGAGGCTGG
1601 CAGGTGGGAG TCTAATGCAG TCAGGAGCAT TTGCATGCAG TGGGTGGAGA
1651 GTCGGCCACC AAAGGACCGA GTTGCGCTCG GAATTTGAGC TGAATTCCAC
1701 AGCCTTACTT TGTTTCCTGA AGTGATAGCC TACTAATGCT GGCAAGCAGA
1751 TGCTTAATAG TAAATTTCTA AAATCCCCGG GTCTTTATCA TTCAGTTTGT
1801 TCTGTGCACC TGAGGCGCTC AGCCGTGGGA GGACCATTTT GCGAGTGTAG
1851 CCCTGTTTCA CTCGGATCAG GTTGGCACGG CCGCCTGCGT GTCTGTCCAC
1901 CTCATCCCTC CGTGTATCTG AGGGAGTAAA GGTGAGGTCT TTATTGCTTC
1951 ACTGCCTAAT TTTCTCACCC ACATTCGCTG AAGCGATGGA GAGTCGGGGG
2001 CCAGTAGCCA GCCAACCCCG TGGGGACCGG GGTTGTCTGT CATTTATGTG
2051 GCTGGAAAGC ACCCAAAGTG GTGGTCAGGA GGGTCGCTGC TGTGGAAGGG
```

```
2101  GTCTCCGTTC TTGGTGCTGT ATTTGAAACG GGTGTAGAGA GAAGCTTGTG
2151  TTTTTGTTTG TAATGGGGAG AAGCGTGGCC AGGCAGGTGG CACGTGGCAT
2201  CGCATGGTGG GCTCGGCAGC ACCTTGCCTG TGTTTCTGTG AGGGAGGCTG
2251  CTTTCTGTGA AATTTCATTT ATATTTTTCT ATTTTTAGTA CTGTATGGAT
2301  GTTACTGAGC ACTACACATG ATCCTTCTGT GCTTGCTTGC ATCTTTAATA
2351  AAGACATGTT CCCGGCGTTG CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2401  AAAAAAAAAA AAAAAAAAA
```

Fig. 11: SEQ ID NO. 4: nucleotide sequence of human SULT4A1 cDNA, splice variant 2

Length: 2080 bp

```
   1  GCGACGGCGA CGGCGGCGGC ATGGCGGAGA GCGAGGCCGA GACCCCCAGC
  51  ACCCCGGGGG AGTTCGAGAG CAAGTACTTC GAGTTCCATG GCGTGCGGCT
 101  GCCGCCCTTC TGCCGCGGGA AGATGGAGGA GATCGCCAAC TTCCCGGTGC
 151  GGCCCAGCGA CGTGTGGATC GTCACCTACC CCAAGTCCGT GGGCTACGGC
 201  TCCTGGTTTG AGCACGTGCA GGAGTTCTGG GAGCACCGCA TGGACTCGAA
 251  CGTGCTTTTT CTCAAGTATG AAGACATGCA TCGGGACCTG GTGACGATGG
 301  TGGAGCAGCT GGCCAGATTC CTGGGGGTGT CCTGTGACAA GGCCCAGCTG
 351  GAAGCCCTGA CGGAGCACTG CCACCAGCTG GTGGACCAGT GCTGCAACGC
 401  TGAGGCCCTG CCCGTGGGCC GGGGAAGAGT TGGGCTGTGG AAGGACATCT
 451  TCACCGTCTC CATGAATGAG AAGTTTGACT TGGTGTATAA ACAGAAGATG
 501  GGAAAGTGTG ACCTCACGTT TGACTTTTAT TTATAATAAC AGAAACAACA
 551  ACCTGCATGC TCACAATACC CAGACAGTCT ACTAGCCAAA AGTCCTGTAT
 601  GCATTCATTT ATTCCTTGCT GGACAAACTC TGGAAGCAGC GTGTGAAACA
 651  GCGGGGGAAG GGAAGAGCGG CGTGAGCGGA GGGAGTGTGA TGATTCCCAA
 701  CCGAAGCAGC TGTCTCGCCT TTAGAACGTG CAGCCTCTCC ATGTCTGATT
 751  ACAAACAGTC TCCACATTGC AGTTCCAATG GCCTGGACCG TAAGGATAAA
 801  GCCTGTAATA TATGCAACTA GAATGTCTGC CTTTTCAACC CCGTATTATT
 851  GTATTTTATA GAGCTTTTCA CTGGAAATCT ACATAAATGT CAGTAAACCA
 901  AATAAAAGTT CATTTCCAAG GGGAATCAGG AGCGAGCCAC ACCCGAATGG
 951  TAGAAAGATC TCAGGGTTAA CTCTTTATTT TTGTAGTTTT ATTATCTAAG
1001  GCACAGCCAT TCTGTTCTCA CTTGGTTCTG AGATAGTGGT GAGAACAGAG
1051  GATGAGTTGG GTCTGTTGGG GGGAATCTGG ACACTTGTTT ATTCTGACGG
1101  AGTTCACTTC TTCAGAACCT TCCTGAAATG AGCAGAAATT GTTCACTAGG
1151  TCTTCAGAAT GGACGTCCTT CTGCCAGAGA CTTCCAGCGG GCGGCTCCAA
1201  AGGCCCAATG CAGAGGAGCC CGCGGAGCAT GTGCTGAGGG AAGTCTGCCT
1251  GGTGAGGCTG GCAGGTGGGA GTCTAATGCA GTCAGGAGCA TTTGCATGCA
1301  GTGGGTGGAG AGTCGGCCAC CAAAGGACCG AGTTGCGCTC GGAATTTGAG
1351  CTGAATTCCA CAGCCTTACT TTGTTTCCTG AAGTGATAGC CTACTAATGC
1401  TGGCAAGCAG ATGCTTAATA GTAAATTTCT AAAATCCCCG GGTCTTTATC
1451  ATTCAGTTTG TTCTGTGCAC CTGAGGCGCT CAGCCGTGGG AGGACCATTT
1501  TGCGAGTGTA GCCCTGTTTC ACTCGGATCA GGTTGGCACG GCCGCCTGCG
1551  TGTCTGTCCA CCTCATCCCT CCGTGTATCT GAGGGAGTAA AGGTGAGGTC
1601  TTTATTGCTT CACTGCCTAA TTTTCTCACC CACATTCGCT GAAGCGATGG
1651  AGAGTCGGGG GCCAGTAGCC AGCCAACCCC GTGGGGACCG GGGTTGTCTG
1701  TCATTTATGT GGCTGGAAAG CACCCAAAGT GGTGGTCAGG AGGGTCGCTG
1751  CTGTGGAAGG GGTCTCCGTT CTTGGTGCTG TATTTGAAAC GGGTGTAGAG
1801  AGAAGCTTGT GTTTTTGTTT GTAATGGGGA GAAGCGTGGC CAGGCAGGTG
1851  GCACGTGGCA TCGCATGGTG GGCTCGGCAG CACCTTGCCT GTGTTTCTGT
1901  GAGGGAGGCT GCTTTCTGTG AAATTTCATT TATATTTTTC TATTTTTAGT
1951  ACTGTATGGA TGTTACTGAG CACTACACAT GATCCTTCTG TGCTTGCTTG
2001  CATCTTTAAT AAAGACATGT TCCCGGCGTT GCAAAAAAAA AAAAAAAAAA
2051  AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
```

Fig. 12: SEQ ID NO. 5

Length: 32 bp

1 GATTGCATCT TTAATAAAGA CATGTTCCCG GC

Fig. 13: SEQ ID NO. 6: nucleotide sequence of human SULT4A1 coding sequence

Length: 855 bp

```
  1  ATGGCGGAGA GCGAGGCCGA GACCCCCAGC ACCCCGGGGG AGTTCGAGAG
 51  CAAGTACTTC GAGTTCCATG GCGTGCGGCT GCCGCCCTTC TGCCGCGGGA
101  AGATGGAGGA GATCGCCAAC TTCCCGGTGC GGCCCAGCGA CGTGTGGATC
151  GTCACCTACC CCAAGTCCGG CACCAGCTTG CTGCAGGAGG TGGTCTACTT
201  GGTGAGCCAG GGCGCTGACC CCGATGAGAT CGGCTTGATG AACATCGACG
251  AGCAGCTCCC GGTCCTGGAG TACCCACAGC CGGGCCTGGA CATCATCAAG
301  GAACTGACCT CTCCCCGCCT CATCAAGAGC CACCTGCCCT ACCGCTTTCT
351  GCCCTCTGAC CTCCACAATG GAGACTCCAA GGTCATCTAT ATGGCTCGCA
401  ACCCCAAGGA TCTGGTGGTG TCTTATTATC AGTTCCACCG CTCTCTGCGG
451  ACCATGAGCT ACCGAGGCAC CTTTCAAGAA TTCTGCCGGA GGTTTATGAA
501  TGATAAGCTG GGCTACGGCT CCTGGTTTGA GCACGTGCAG GAGTTCTGGG
551  AGCACCGCAT GGACTCGAAC GTGCTTTTTC TCAAGTATGA AGACATGCAT
601  CGGGACCTGG TGACGATGGT GGAGCAGCTG GCCAGATTCC TGGGGGTGTC
651  CTGTGACAAG GCCCAGCTGG AAGCCCTGAC GGAGCACTGC CACCAGCTGG
701  TGGACCAGTG CTGCAACGCT GAGGCCCTGC CCGTGGGCCG GGGAAGAGTT
751  GGGCTGTGGA AGGACATCTT CACCGTCTCC ATGAATGAGA AGTTTGACTT
801  GGTGTATAAA CAGAAGATGG GAAAGTGTGA CCTCACGTTT GACTTTTATT
851  TATAA
```

Fig. 14: Alignment of SEQ ID NO. 5 with human SULT4A1sv1 and SULT4A1sv2 cDNAs

Length: 32 bp

SEQ ID NO.5 : SULT4A1sv1

```
   1 GATTGCATCTTTAATAAAGACATGTTCCCGGC 32
     | ||||||||||||||||||||||||||||||
2335 GCTTGCATCTTTAATAAAGACATGTTCCCGGC 2366
```

SEQ ID NO.5 : SULT4A1sv2

```
   1 GATTGCATCTTTAATAAAGACATGTTCCCGGC 32
     | ||||||||||||||||||||||||||||||
1996 GCTTGCATCTTTAATAAAGACATGTTCCCGGC 2027
```

Fig. 15 :

Samples	Controls													
Braak stage	0		1		2		3		4		5		6	
	C011	F1.37	C005	F1.12	C008	F1.20	C025	T1.07	P012	F2.27	P010	F7.14	P014	F2.04
	C012	F1.20	C014	T2.38	C031	[illegible]	C035	F1.20	P016	[illegible]	P011	F2.86	P017	[illegible]
	C026	T1.02	C028	F1.09	C033	[illegible]	DE05	F2.50	P038	F2.44	P040	F3.03	P019	F2.30
	C027	T1.17	C029	F1.27	C034	F1.09	DE07	[illegible]	P046	F2.70	P041	F3.23	P042	F2.17
	C032	F1.16	C030	F1.18	C041	F1.11			P047	[illegible]	P048	F1.27		
			C036	F1.33	C042	T1.10					P049	[illegible]		
			C038	[illegible]	DE02	F1.35								
			C039	T1.11	DE03	T1.17								

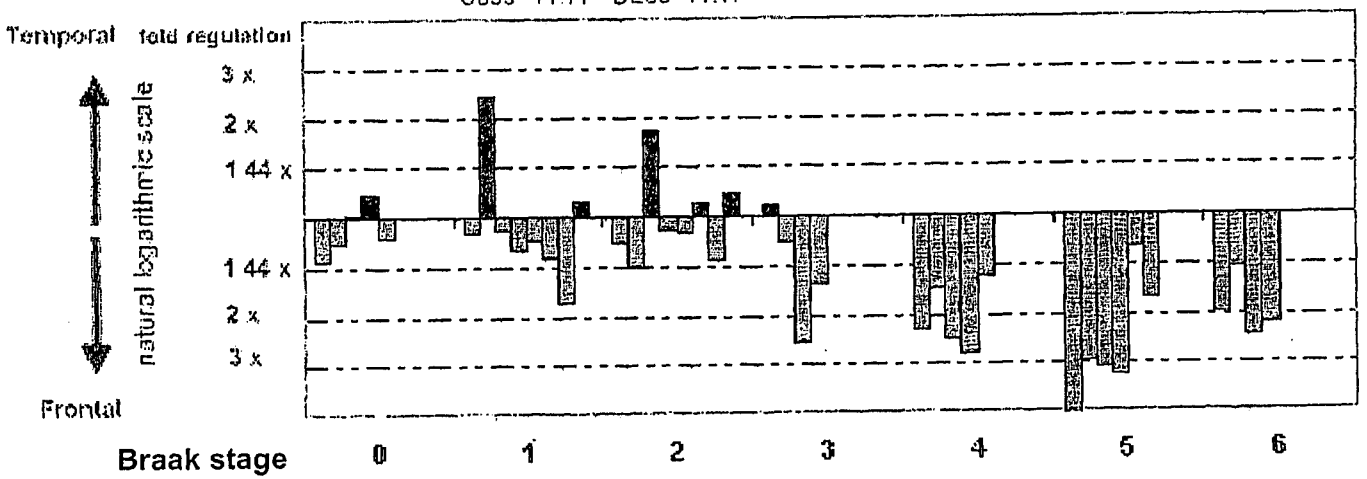


Fig. 16 :

Samples	Controls										AD Patients											
Braak stage	0		1		2		3		4		5		6									
	C011	F2.27	C005	T1.44	C008	F2.00	C025	F2.33	P012	F4.17	P010	F7.69	P014	[illegible]								
	C012	[illegible]	C014	[illegible]	C031	F2.17	C035	[illegible]	P016	F5.00	P011	F3.57	P017	F12.50								
	C026	F1.15	C028	[illegible]	C033		DE05	F3.33	P038	F10.00	P040	F4.76	P019	F16.67								
	C027	T1.36	C029	F1.25	C034	[illegible]	DE07	[illegible]	P046	F2.33	P041	F9.09	P042	F2.94								
	C032	F2.17	C030	F1.35	C041	F1.03			P047	[illegible]	P048	F1.10										
			C036	[illegible]	C042	F1.30					P049	F1.35										
			C038	F1.33	DE02	F3.33																
			C039	T1.14	DE03	T3.45																

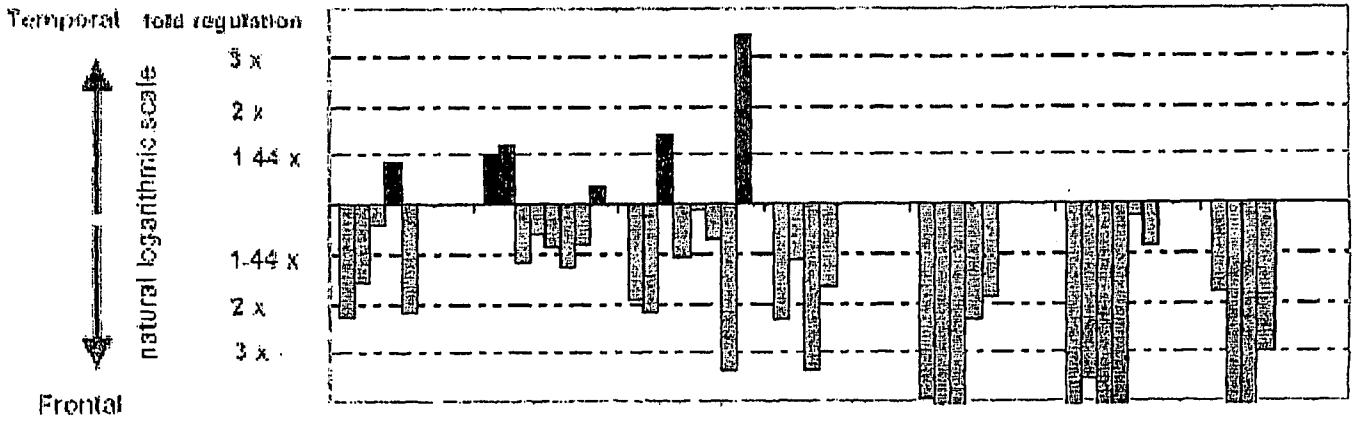
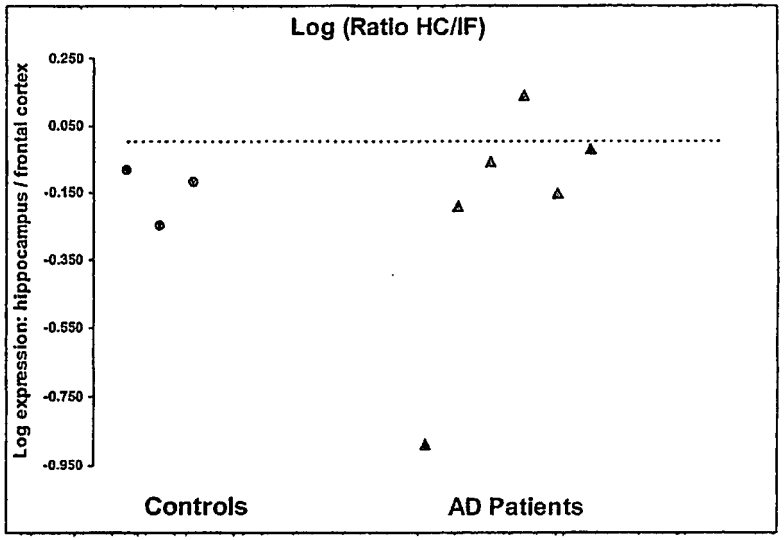


Fig. 17 :

sample	Δ (fold) (hippocampus/ frontal cortex)
control C004	0.82
control C005	0.56
control C008	0.76
patient P010	0.13
patient P011	0.64
patient P012	0.87
patient P014	1.37
patient P016	0.70
patient P019	0.95



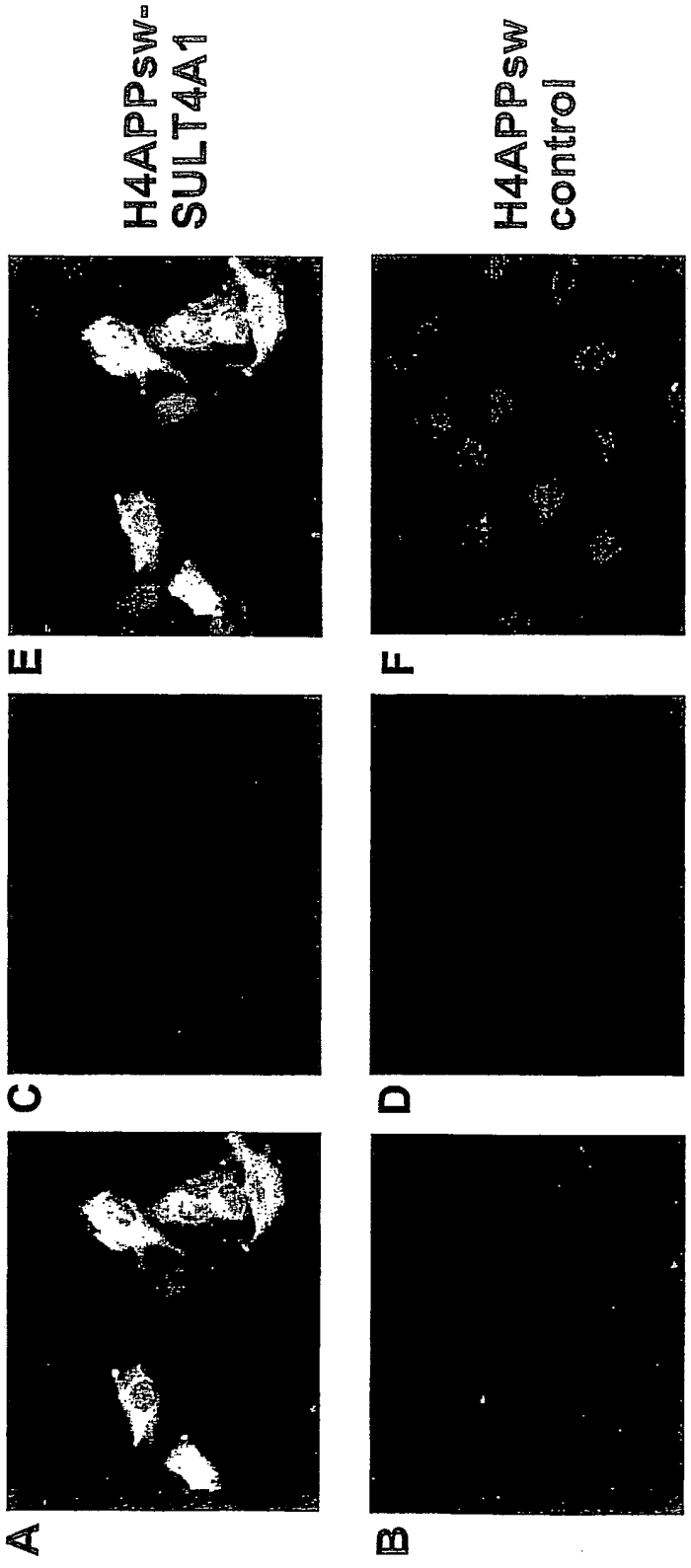


Fig. 18: Immunofluorescence analysis of SULT4A1 protein in neuroglioma cells

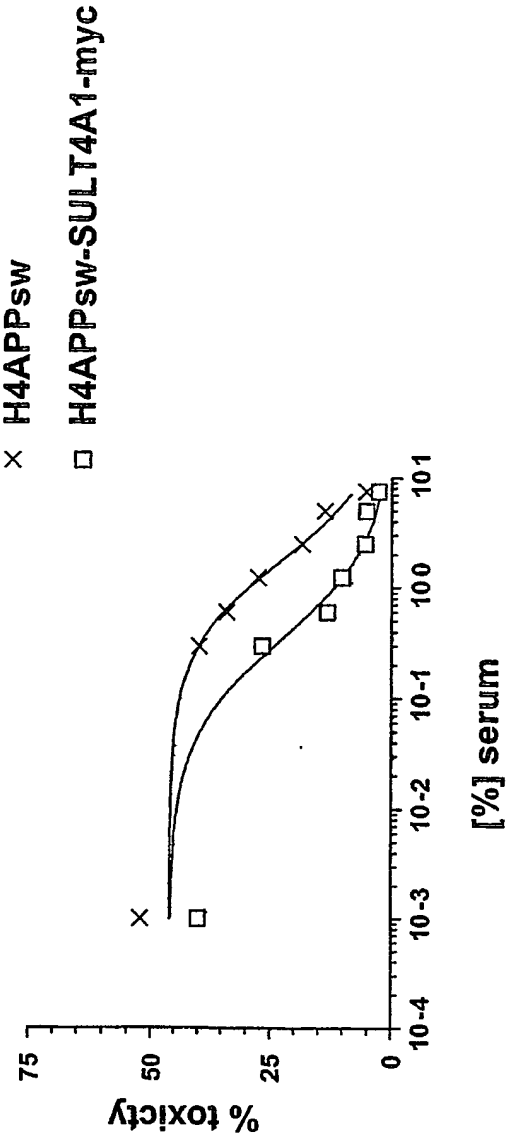


Fig. 19: Effect of trophic factor deprivation on SULT4A1 over-expressing cells

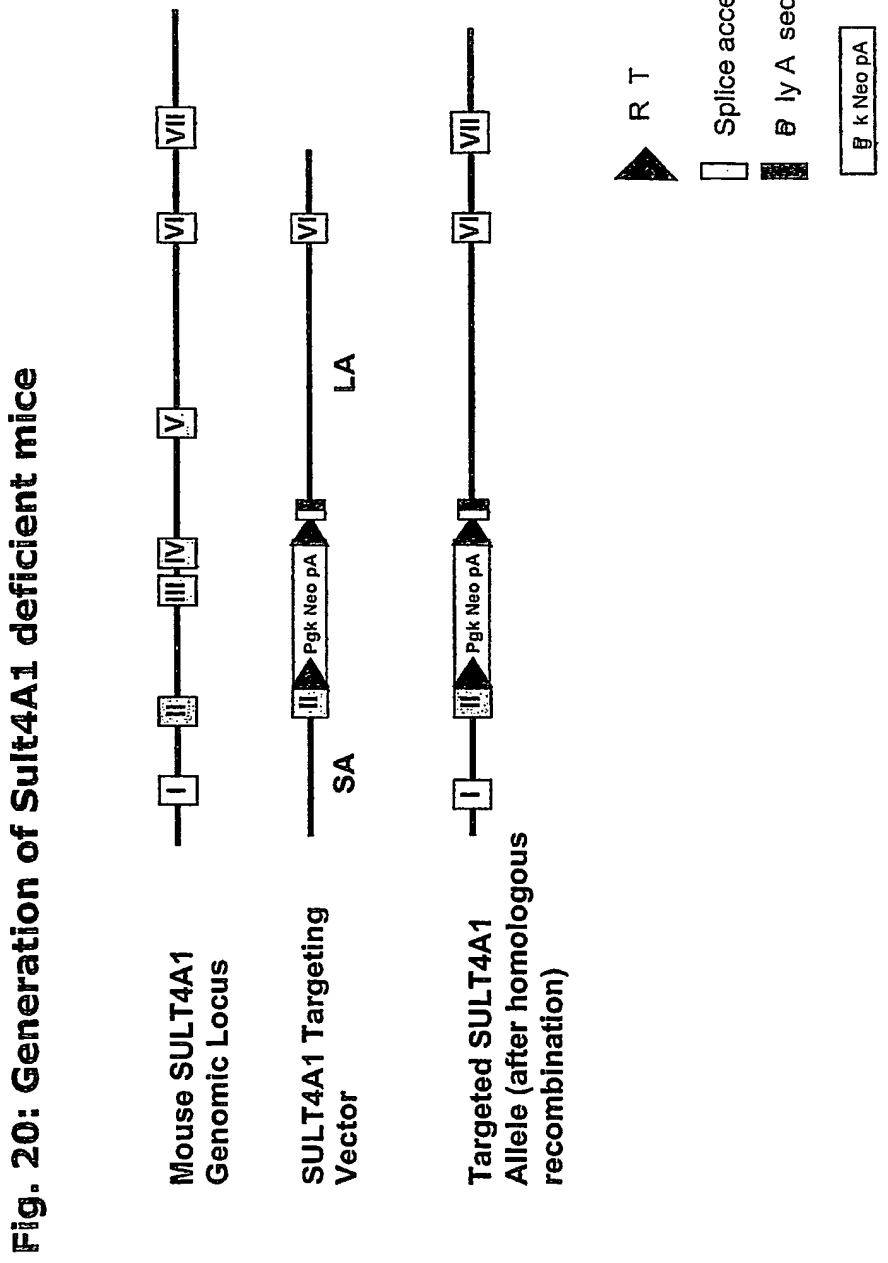


Fig. 20: Generation of Sult4A1 deficient mice

Fig. 21: Generation of Sult4A1 trangenic mice

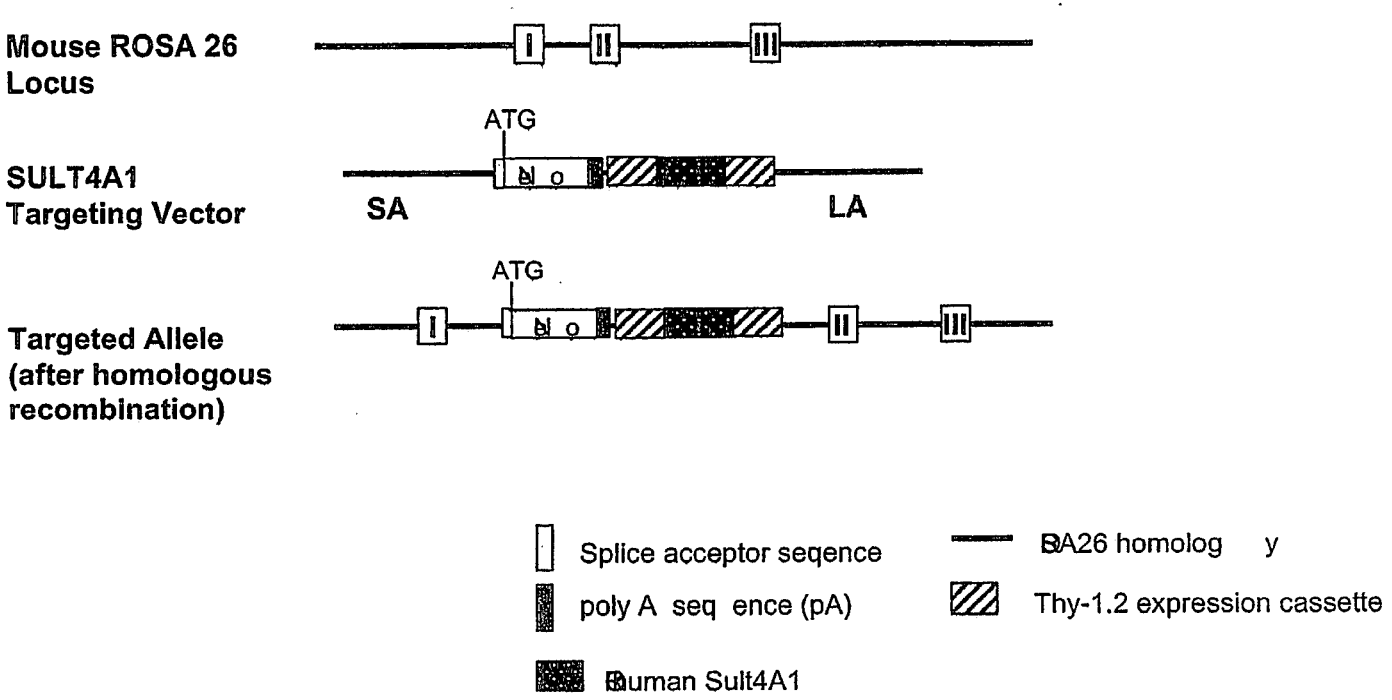
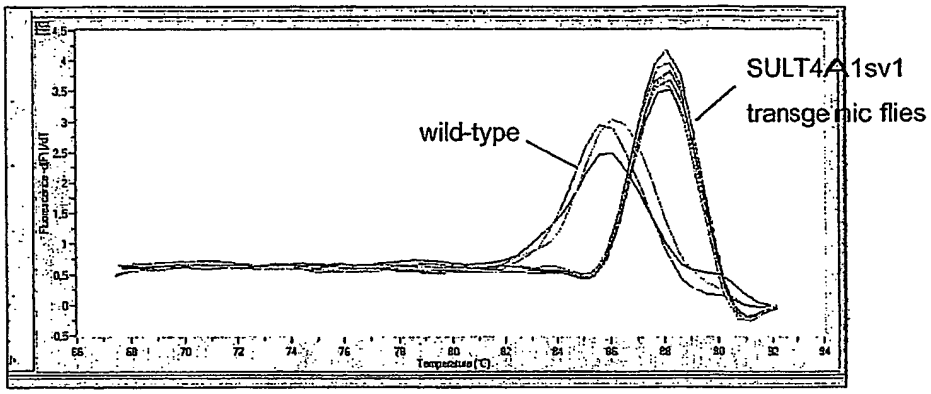


Fig. 22: Transgenic expression of Sult4A1

A



B

name	cycle number	mean	stdev	error [%]	efficiency (expression normalized to housekeeping gene)
SULT4A1#3	21.34	21.300	0.14422205	0.67709883	1.8 times more than SULT4A1#8; 2.7 times more than SULT4A1#22
SULT4A1#3	21.14				
SULT4A1#3	21.42				
SULT4A1#8	23.79	23.917	0.11676187	0.48820292	
SULT4A1#8	23.94				
SULT4A1#8	24.02				
SULT4A1#22		23.915	0.03535534	0.1478375	
SULT4A1#22	23.94				
SULT4A1#22	23.89				

$E = 10^{(-1/slope)}$ slope= -2.960 E= 2.176

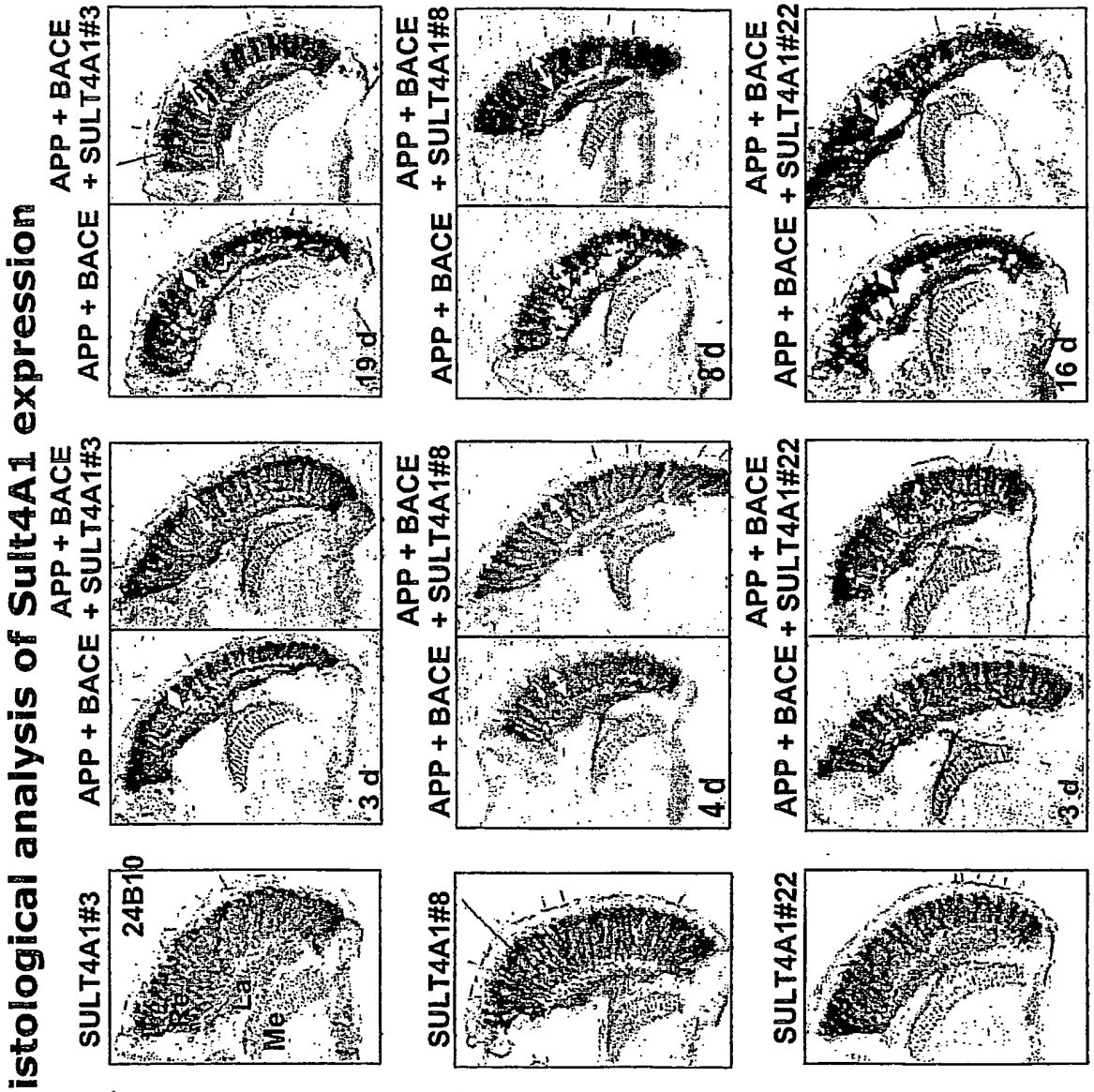


Fig. 23: Histological analysis of Sult4A1 expression

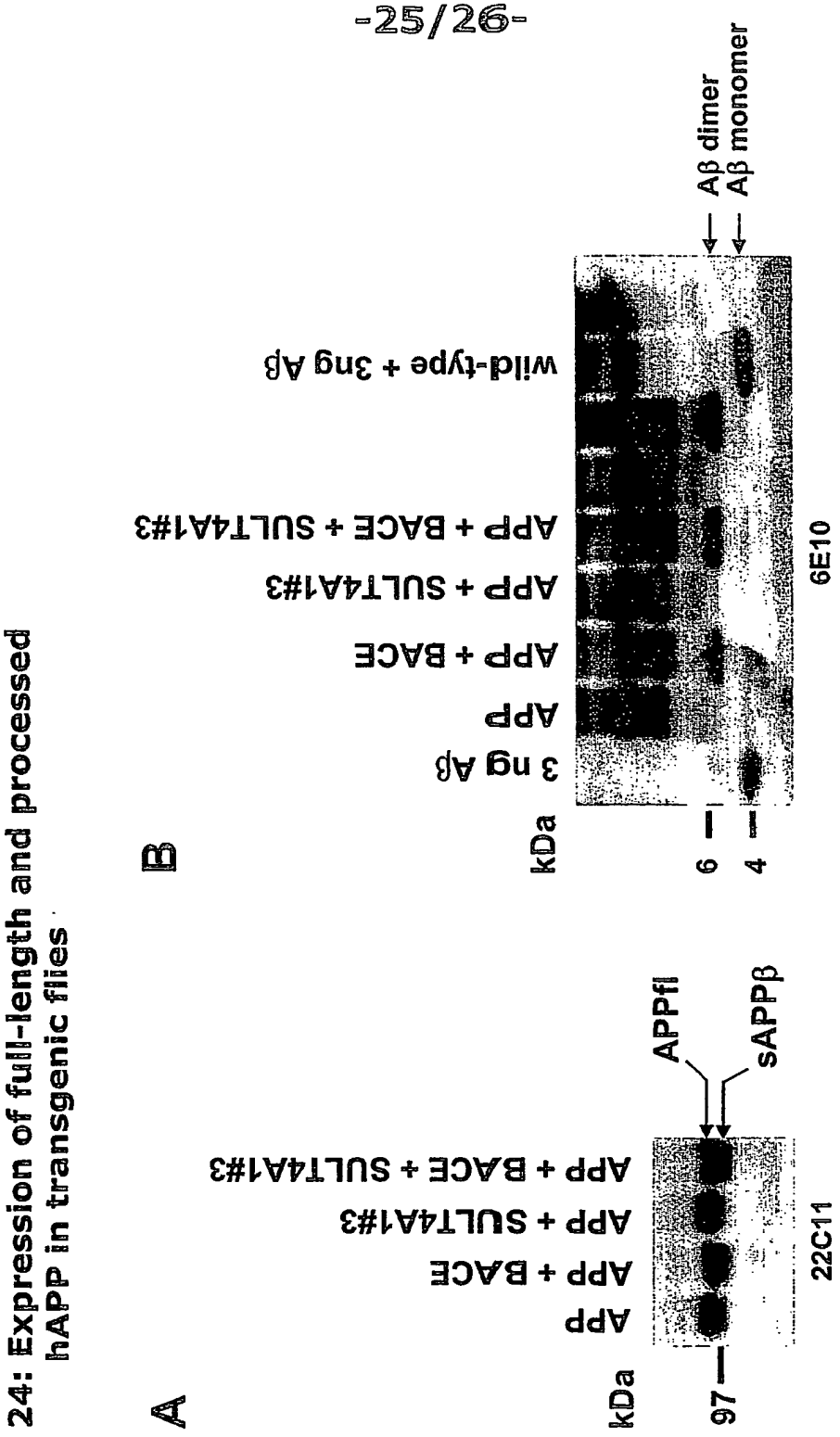


Fig. 24: Expression of full-length and processed hAPP in transgenic flies

Fig. 25: Thioflavin S positive amyloid plaques in transgenic flies